

=> d que

L1 7 SEA FILE=REGISTRY ABB=ON PLU=ON DQLGDWMLNYFRLVPPGT/SQSP
 L2 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L1

=> d 12 ibib abs hitind

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 2004:267260 HCAPLUS
 DOCUMENT NUMBER: 140:297533
 TITLE: Peptides and related molecules that modulate nerve
 growth factor activity
 INVENTOR(S): Boone, Thomas C.; Wild, Kenneth D., Jr.; Sitney, Karen
 C.; Min, Hosung; Kimmel, Bruce
 PATENT ASSIGNEE(S): Amgen Inc., USA
 SOURCE: PCT Int. Appl., 267 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004026329	A1	20040401	WO 2003-US29866	20030919
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004121959	A1	20040624	US 2003-666480	20030918
PRIORITY APPLN. INFO.:			US 2002-412524P	P 20020919
			US 2003-666480	A 20030918

OTHER SOURCE(S): MARPAT 140:297533

AB The present invention relates to certain biol. active peptides and polypeptides which can be used as therapeutics or prophylactics against diseases or disorders linked to nerve growth factor (NGF) as the causative agent. In one aspect of the present invention, pharmacol. active polypeptides comprising peptides linked to one or more Fc domains are provided.

IC ICM A61K038-10
 ICS A61K038-16; C07H021-04; C07K007-08; C07K014-00

CC 1-11 (Pharmacology)

IT 57-88-5D, Cholesterol, conjugates with peptides 7093-67-6D, conjugates with peptides and Fc domains 18861-82-0D, conjugates with peptides and Fc domains 25322-68-3D, Polyethylene glycol, conjugates with peptides 676329-46-7D, linker-peptide-Fc domain conjugates 676329-48-9D, linker-peptide-Fc domain conjugates 676329-50-3D, linker-peptide-Fc domain conjugates 676329-51-4D, linker-peptide-Fc domain conjugates 676329-53-6D, linker-peptide-Fc domain conjugates 676329-54-7D, linker-peptide-Fc domain conjugates 676329-55-8D, linker-peptide-Fc

conjugates 676330-68-0D, linker-peptide-Fc domain conjugates
676330-69-1D, linker-peptide-Fc domain conjugates 676330-70-4
676330-70-4D, linker-peptide-Fc domain conjugates 676330-71-5D,
linker-peptide-Fc domain conjugates 676330-72-6D, linker-peptide-Fc
domain conjugates 676330-73-7D, linker-peptide-Fc domain conjugates
676330-74-8 676330-74-8D, linker-peptide-Fc domain conjugates
676330-75-9D, linker-peptide-Fc domain conjugates 676330-76-0
676330-76-0D, linker-peptide-Fc domain conjugates **676330-77-1**
676330-77-1D, linker-peptide-Fc domain conjugates 676330-78-2
676330-78-2D, linker-peptide-Fc domain conjugates 676330-79-3
676330-79-3D, linker-peptide-Fc domain conjugates 676330-80-6
676330-80-6D, linker-peptide-Fc domain conjugates 676330-81-7D,
linker-peptide-Fc domain conjugates 676330-82-8 676330-82-8D,
linker-peptide-Fc domain conjugates **676330-83-9**
~~676330-83-9D~~, linker-peptide-Fc domain conjugates 676330-84-0D,
linker-peptide-Fc domain conjugates 676330-85-1 676330-85-1D,
linker-peptide-Fc domain conjugates 676330-86-2 676330-86-2D,
linker-peptide-Fc domain conjugates 676330-87-3 676330-87-3D,
linker-peptide-Fc domain conjugates 676330-88-4D, linker-peptide-Fc
domain conjugates 676330-89-5D, linker-peptide-Fc domain conjugates
676330-90-8D, linker-peptide-Fc domain conjugates 676330-91-9D,
linker-peptide-Fc domain conjugates 676330-92-0 676330-92-0D,
linker-peptide-Fc domain conjugates 676330-93-1 676330-93-1D,
linker-peptide-Fc domain conjugates 676330-94-2D, linker-peptide-Fc
domain conjugates 676330-95-3D, linker-peptide-Fc domain conjugates
676330-96-4D, linker-peptide-Fc domain conjugates 676330-97-5
676330-97-5D, linker-peptide-Fc domain conjugates 676330-98-6D,
linker-peptide-Fc domain conjugates 676330-99-7D, linker-peptide-Fc
domain conjugates 676331-00-3D, linker-peptide-Fc domain conjugates
676331-01-4D, linker-peptide-Fc domain conjugates 676331-02-5D,
linker-peptide-Fc domain conjugates 676331-03-6D, linker-peptide-Fc
domain conjugates 676331-04-7D, linker-peptide-Fc domain conjugates
676331-05-8 676331-05-8D, linker-peptide-Fc domain conjugates
676331-06-9D, linker-peptide-Fc domain conjugates 676331-07-0D,
linker-peptide-Fc domain conjugates 676331-08-1D, linker-peptide-Fc
domain conjugates 676331-10-5D, linker-peptide-Fc domain conjugates
676331-11-6D, linker-peptide-Fc domain conjugates 676331-12-7D,
linker-peptide-Fc domain conjugates 676331-13-8 676331-13-8D,
linker-peptide-Fc domain conjugates 676331-14-9D, linker-peptide-Fc
domain conjugates 676331-15-0D, linker-peptide-Fc domain conjugates
676331-16-1D, linker-peptide-Fc domain conjugates 676331-17-2D,
linker-peptide-Fc domain conjugates 676331-18-3D, linker-peptide-Fc
domain conjugates **676331-19-4 676331-19-4D**,
linker-peptide-Fc domain conjugates 676331-20-7 676331-20-7D,
linker-peptide-Fc domain conjugates 676331-21-8 676331-21-8D,
linker-peptide-Fc domain conjugates 676331-22-9 676331-22-9D,
linker-peptide-Fc domain conjugates 676373-30-1D, linker-peptide-Fc
domain conjugates 676373-31-2D, linker-peptide-Fc domain conjugates
676373-32-3D, linker-peptide-Fc domain conjugates 676373-33-4D,
conjugates with peptides 676373-34-5 676373-35-6
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(peptides and related mols. that modulate nerve growth factor activity
linked to vehicles such as antibody Fc domains for treatment of
diseases associated with pain)

REFERENCE COUNT:

2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

Russel 10/666,480

01/07/2005

L1 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2005 ACS on STN
RN 676331-19-4 REGISTRY
CN L-Leucine, L-alanyl-L-glutaminyl-L-prolyl-L-threonyl-L- α -aspartyl-L-
glutaminyl-L-leucylglycyl-L- α -aspartyl-L-tryptophyl-L-methionyl-L-
leucyl-L-asparaginyl-L-tyrosyl-L-phenylalanyl-L-arginyl-L-leucyl-L-valyl-L-
proyl-L-prolylglycyl-L-threonyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 61: PN: WO2004026329 SEQID: 272 claimed DNA
SQL 23

SEQ 1 AQPTDQLG DW MLNYFRLVPP GTL
===== ===== ==

HITS AT: 5-22
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L1 ANSWER 2 OF 7 REGISTRY COPYRIGHT 2005 ACS on STN
RN 676330-83-9 REGISTRY
CN L-Glutamic acid, L-prolyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-
leucylglycyl-L- α -aspartyl-L-tryptophyl-L-methionyl-L-leucyl-L-
asparaginyl-L-tyrosyl-L-phenylalanyl-L-arginyl-L-leucyl-L-valyl-L-proyl-L-
prolylglycyl-L-threonyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 383: PN: WO2004026329 SEQID: 237 claimed sequence
SQL 22

SEQ 1 PTDQLGDWML NYFRLVPPGT LE
===== =====

HITS AT: 3-20
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L1 ANSWER 3 OF 7 REGISTRY COPYRIGHT 2005 ACS on STN
RN 676330-77-1 REGISTRY
CN L-Threonine, L- α -aspartyl-L-glutaminyl-L-leucylglycyl-L- α -
aspartyl-L-tryptophyl-L-methionyl-L-leucyl-L-asparaginyl-L-tyrosyl-L-
phenylalanyl-L-arginyl-L-leucyl-L-valyl-L-proyl-L-prolylglycyl- (9CI).
(CA INDEX NAME)

OTHER NAMES:

CN 377: PN: WO2004026329 SEQID: 231 claimed sequence
SQL 18

SEQ 1 DQLGDWMLNY FRLVPPGT
===== =====

HITS AT: 1-18
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L1 ANSWER 4 OF 7 REGISTRY COPYRIGHT 2005 ACS on STN
RN 676330-67-9 REGISTRY
CN L-Threonine, L-prolyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-
leucylglycyl-L- α -aspartyl-L-tryptophyl-L-methionyl-L-leucyl-L-
asparaginyl-L-tyrosyl-L-phenylalanyl-L-arginyl-L-leucyl-L-valyl-L-proyl-L-
prolylglycyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 367: PN: WO2004026329 SEQID: 221 claimed sequence
SQL 20

SEQ 1 PTDQLGDWML NYFRLVPPGT

===== =====
HITS AT: 3-20
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L1 ANSWER 5 OF 7 REGISTRY COPYRIGHT 2005 ACS on STN
RN 676330-65-7 REGISTRY
CN L-Glutamic acid, L-alanyl-L-glutaminyl-L-prolyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-leucylglycyl-L- α -aspartyl-L-tryptophyl-L-methionyl-L-leucyl-L-asparaginyl-L-tyrosyl-L-phenylalanyl-L-arginyl-L-leucyl-L-valyl-L-prolyl-L-prolylglycyl-L-threonyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 365: PN: WO2004026329 SEQID: 219 claimed sequence
SQL 24

SEQ 1 AQPTDQLGDW MLNYFRLVPP GTLE
===== ===== =

HITS AT: 5-22
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L1 ANSWER 6 OF 7 REGISTRY COPYRIGHT 2005 ACS on STN
RN 676330-57-7 REGISTRY
CN L-Glutamic acid, L-glutaminyl-L-prolyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-leucylglycyl-L- α -aspartyl-L-tryptophyl-L-methionyl-L-leucyl-L-asparaginyl-L-tyrosyl-L-phenylalanyl-L-arginyl-L-leucyl-L-valyl-L-prolyl-L-prolylglycyl-L-threonyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 357: PN: WO2004026329 SEQID: 211 claimed sequence
SQL 23

SEQ 1 QPTDQLGDWM LNYFRLVPPG TLE
===== ===== =

HITS AT: 4-21
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L1 ANSWER 7 OF 7 REGISTRY COPYRIGHT 2005 ACS on STN
RN 676330-48-6 REGISTRY
CN L-Threonine, L-alanyl-L-glutaminyl-L-prolyl-L-threonyl-L- α -aspartyl-L-glutaminyl-L-leucylglycyl-L- α -aspartyl-L-tryptophyl-L-methionyl-L-leucyl-L-asparaginyl-L-tyrosyl-L-phenylalanyl-L-arginyl-L-leucyl-L-valyl-L-prolyl-L-prolylglycyl- (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 348: PN: WO2004026329 SEQID: 202 claimed sequence
SQL 22

SEQ 1 AQPTDQLGDW MLNYFRLVPP GT
===== ===== =

HITS AT: 5-22
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2005, 15:34:01 ; Search time 62 Seconds
(without alignments)
167.044 Million cell updates/sec

Title: US-10-666-480-231
Perfect score: 104
Sequence: 1 DQLGDWMLNYFRLVPPGT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	52	50.0	243	2	Q9PJC8	Q9pjc8 chlamydia m
2	50	48.1	343	2	Q8GW08	Q8gw08 oryza sativ
3	50	48.1	343	2	BAC83487	Bac83487 oryza sat
4	50	48.1	518	2	Q9VLU7	Q9vlu7 drosophila
5	50	48.1	552	2	Q96VC4	Q96vc4 emericella
6	50	48.1	762	2	Q6R7C7	Q6r7c7 ostreid her
7	50	48.1	762	2	AAS00988	Aas00988 ostreid h
8	48	46.2	243	2	O84617	O84617 chlamydia t
9	48	46.2	297	2	Q82MC4	Q82mc4 streptomyce
10	48	46.2	896	1	NAH5_HUMAN	Q14940 homo sapien
11	47.5	45.7	473	2	Q88BC1	Q88bc1 pseudomonas
12	47.5	45.7	496	2	Q88CA6	Q88ca6 pseudomonas
13	47	45.2	405	2	O66181	O66181 arthrobacte
14	47	45.2	419	1	RNBP_RAT	P51607 rattus norv
15	47	45.2	514	2	Q8GM94	Q8gm94 serratia ma

16	47	45.2	891	2	Q7N4B7	Q7n4b7 photorhabdu
17	47	45.2	903	2	Q9A299	Q9a299 caulobacter
18	46	44.2	215	2	Q6QH48	Q6qh48 anticarsia
19	46	44.2	215	2	AAS83209	Aas83209 anticarsi
20	46	44.2	315	2	Q9SKN6	Q9skn6 arabidopsis
21	46	44.2	362	2	Q8FND8	Q8fnd8 corynebacte
22	46	44.2	405	2	Q91WI9	Q91wi9 mus musculu
23	46	44.2	417	1	RNBP_HUMAN	P51606 homo sapien
24	46	44.2	419	1	RNBP_MOUSE	P82343 mus musculu
25	46	44.2	464	2	Q9KEM8	Q9kem8 bacillus ha
26	46	44.2	554	2	Q7RXW8	Q7rxw8 neurospora
27	46	44.2	1394	2	Q7Q971	Q7q971 anopheles g
28	46	44.2	2042	2	Q7Q3U4	Q7q3u4 anopheles g
29	45.5	43.8	183	2	Q89K86	Q89k86 bradyrhizob
30	45.5	43.8	1202	2	Q7WF28	Q7wf28 bordetella
31	45.5	43.8	1224	2	Q7W3Q1	Q7w3q1 bordetella
32	45	43.3	142	2	Q9S2F7	Q9s2f7 streptomyce
33	45	43.3	331	2	Q6C1P0	Q6c1p0 yarrowia li
34	45	43.3	359	2	Q8RIS8	Q8ris8 actinoplane
35	45	43.3	453	2	Q8EKN5	Q8ekn5 shewanella
36	45	43.3	878	1	ACON_RICCN	Q92g90 rickettsia
37	45	43.3	878	1	ACON_RICPR	Q9zcf4 rickettsia
38	45	43.3	878	2	Q7P9X6	Q7p9x6 rickettsia
39	45	43.3	890	2	Q83B05	Q83b05 coxiella bu
40	45	43.3	928	2	Q6FUJ3	Q6fuj3 candida gla
41	44.5	42.8	100	2	Q7UZC7	Q7uzc7 rhodopirell
42	44.5	42.8	324	2	Q876L8	Q87618 trichoderma
43	44.5	42.8	421	2	Q9GRS9	Q9grs9 leishmania
44	44.5	42.8	486	2	Q00995	Q00995 kluyveromyc
45	44.5	42.8	486	2	Q6CWY3	Q6cwy3 kluyveromyc

ALIGNMENTS

RESULT 1

Q9PJC8

ID Q9PJC8 PRELIMINARY; PRT; 243 AA.
 AC Q9PJC8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein TC0901.
 GN OrderedLocusNames=TC0901;
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MoPn / Nigg;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
 RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
 RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
 RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia

RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002356; AAF39694.1; -.
DR PIR; E81652; E81652.
DR TIGR; TC0901; -.
DR InterPro; IPR002847; DUF129.
DR InterPro; IPR008225; UCP005026.
DR Pfam; PF01996; DUF129; 1.
DR PIRSF; PIRSF005026; UCP005026; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 243 AA; 27135 MW; 3CF6BD1258A47802 CRC64;

Query Match 50.0%; Score 52; DB 2; Length 243;
Best Local Similarity 53.8%; Pred. No. 6.9;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQLGDWMLNYFRL 13
:|:|:|: ||||:
Db 110 NQIGEWLKNYFRV 122

Search completed: January 7, 2005, 16:05:32
Job time : 65 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2005, 15:52:11 ; Search time 16 Seconds
(without alignments)
108.244 Million cell updates/sec

Title: US-10-666-480-231
Perfect score: 104
Sequence: 1 DQLGDWMLNYFRLVPPGT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	52	50.0	243	2	E81652	conserved hypothet
2	50	48.1	552	2	JC7666	serine-type carbox
3	48	46.2	243	1	G71493	hypothetical prote
4	47	45.2	405	2	T44249	transport protein
5	47	45.2	419	2	JX0187	renin-binding prot
6	47	45.2	903	2	A87704	aconitate hydratas
7	46	44.2	315	2	F84683	hypothetical prote
8	46	44.2	417	2	JX0188	renin-binding prot
9	46	44.2	464	2	H83752	glutamate dehydrog
10	45	43.3	142	2	T36147	probable regulator
11	45	43.3	878	2	A97854	aconitate hydratas
12	45	43.3	878	2	A71641	aconitate hydratas
13	44.5	42.8	486	2	S72516	FOG1 protein - yea

14	44	42.3	944	2	G87135	aconitate hydratas
15	44	42.3	1272	2	T37807	hypothetical prote
16	43	41.3	137	2	G95352	protein [imported
17	43	41.3	173	2	C86503	acyltransferase [i
18	43	41.3	246	2	A72040	ct611 hypothetical
19	43	41.3	246	2	F86585	CT611 hypothetical
20	43	41.3	246	2	A81502	conserved hypothet
21	43	41.3	273	2	S75316	phycocyanin-associ
22	43	41.3	507	2	T31975	hypothetical prote
23	43	41.3	1270	2	T09194	adaptor protein in
24	42.5	40.9	219	2	B75533	hypothetical prote
25	42.5	40.9	402	2	AG0638	probable membrane
26	42.5	40.9	412	2	F64849	probable permease
27	42.5	40.9	412	2	C99809	hypothetical prote
28	42.5	40.9	668	2	AG1989	hypothetical prote
29	42.5	40.9	780	2	G72724	probable penicilli
30	42	40.4	411	2	B71451	probable desucciny
31	42	40.4	418	2	B72245	conserved hypothet
32	42	40.4	420	2	AB0246	glutamyl-tRNA redu
33	42	40.4	552	2	G69464	acetolactate synth
34	42	40.4	742	2	H95270	probable kinase/es
35	42	40.4	763	2	A29562	PRT1 protein - yea
36	42	40.4	810	2	T33323	hypothetical prote
37	42	40.4	890	2	AH0270	aconitate hydratas
38	42	40.4	895	2	AI3483	aconitate hydratas
39	42	40.4	897	2	AD2906	aconitate hydratas
40	42	40.4	897	2	E97681	aconitate hydratas
41	41.5	39.9	412	2	G85668	hypothetical prote
42	41.5	39.9	796	2	D97065	transketolase [imp
43	41	39.4	165	2	T46052	ADP-ribosylation f
44	41	39.4	321	2	AH2766	conserved hypothet
45	41	39.4	321	2	C97547	hypothetical prote

ALIGNMENTS

RESULT 1

E81652

conserved hypothetical protein TC0901 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Dec-2002

C;Accession: E81652

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser, C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-243 <TET>

A;Cross-references: GB:AE002356; GB:AE002160; NID:g7190921; PIDN:AAF39694.1;
PID:g7190928; GSPDB:GN00121; TIGR:TC0901
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0901
C;Superfamily: uncharacterized conserved protein

Query Match 50.0%; Score 52; DB 2; Length 243;
Best Local Similarity 53.8%; Pred. No. 0.94;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQLGDWMLNYFRL 13
:|:|:|: ||||:
Db 110 NQIGEWLKNYFRV 122

Search completed: January 7, 2005, 16:08:34
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2005, 16:08:22 ; Search time 145 Seconds
(without alignments)
44.761 Million cell updates/sec

Title: US-10-666-480-231
Perfect score: 104
Sequence: 1 DQLGDWMLNYFRLVPPGT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	104	100.0	18	16	US-10-666-480-231	Sequence 231, App
2	104	100.0	20	16	US-10-666-480-221	Sequence 221, App
3	104	100.0	22	16	US-10-666-480-202	Sequence 202, App
4	104	100.0	22	16	US-10-666-480-237	Sequence 237, App
5	104	100.0	23	16	US-10-666-480-211	Sequence 211, App
6	104	100.0	23	16	US-10-666-480-272	Sequence 272, App
7	104	100.0	24	16	US-10-666-480-219	Sequence 219, App
8	99	95.2	19	16	US-10-666-480-227	Sequence 227, App
9	54	51.9	26	16	US-10-666-480-271	Sequence 271, App
10	51	49.0	67	17	US-10-425-115-316169	Sequence 316169,
11	50	48.1	26	16	US-10-666-480-226	Sequence 226, App
12	50	48.1	343	16	US-10-437-963-193691	Sequence 193691,
13	50	48.1	429	14	US-10-369-493-13233	Sequence 13233, A
14	49	47.1	344	9	US-09-999-672-11	Sequence 11, Appl
15	49	47.1	344	13	US-10-040-863-11	Sequence 11, Appl
16	48	46.2	22	16	US-10-666-480-251	Sequence 251, App
17	48	46.2	207	9	US-09-841-132-300	Sequence 300, App
18	48	46.2	207	17	US-10-872-155-300	Sequence 300, App
19	48	46.2	243	9	US-09-841-132-579	Sequence 579, App
20	48	46.2	243	17	US-10-872-155-579	Sequence 579, App
21	48	46.2	249	9	US-09-841-132-365	Sequence 365, App
22	48	46.2	249	17	US-10-872-155-365	Sequence 365, App
23	48	46.2	297	14	US-10-156-761-9275	Sequence 9275, Ap
24	48	46.2	896	14	US-10-217-096-6	Sequence 6, Appli
25	48	46.2	896	16	US-10-408-765A-620	Sequence 620, App
26	48	46.2	896	17	US-10-757-262-114	Sequence 114, App
27	48	46.2	896	17	US-10-768-158-36	Sequence 36, Appl
28	47	45.2	26	16	US-10-666-480-239	Sequence 239, App
29	47	45.2	179	15	US-10-424-599-162543	Sequence 162543,
30	47	45.2	882	14	US-10-369-493-7994	Sequence 7994, Ap
31	47	45.2	891	14	US-10-369-493-21094	Sequence 21094, A
32	47	45.2	896	14	US-10-369-493-209	Sequence 209, App
33	47	45.2	903	14	US-10-369-493-17080	Sequence 17080, A
34	46	44.2	145	16	US-10-767-701-55257	Sequence 55257, A
35	46	44.2	291	14	US-10-286-264-98	Sequence 98, Appl
36	46	44.2	291	15	US-10-412-699B-916	Sequence 916, App
37	46	44.2	417	14	US-10-116-275-224	Sequence 224, App
38	46	44.2	464	14	US-10-369-493-17155	Sequence 17155, A
39	46	44.2	539	14	US-10-369-493-3911	Sequence 3911, Ap
40	45.5	43.8	1292	16	US-10-437-963-188422	Sequence 188422,
41	45	43.3	211	17	US-10-425-115-358149	Sequence 358149,
42	45	43.3	887	14	US-10-369-493-17785	Sequence 17785, A
43	44.5	42.8	1592	16	US-10-437-963-188419	Sequence 188419,
44	44.5	42.8	1975	16	US-10-437-963-188418	Sequence 188418,
45	44	42.3	21	16	US-10-666-480-210	Sequence 210, App

ALIGNMENTS

RESULT 1

US-10-666-480-231
; Sequence 231, Application US/10666480
; Publication No. US20040121959A1

; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Sitney, Karen C
; APPLICANT: Min, Hosung
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor Activity
; FILE REFERENCE: A-827US
; CURRENT APPLICATION NUMBER: US/10/666,480
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 231
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Therapeutically active peptide of randomly generated, non-natural
; OTHER INFORMATION: lly occurring sequence
US-10-666-480-231

Query Match 100.0%; Score 104; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQLGDWMLNYFRLVPPGT 18
||| ||| ||| ||| ||| |||
Db 1 DQLGDWMLNYFRLVPPGT 18

RESULT 10
US-10-425-115-316169
; Sequence 316169, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 316169
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(67)

; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_51416C.1.pep
US-10-425-115-316169

Query Match 49.0%; Score 51; DB 17; Length 67;
Best Local Similarity 50.0%; Pred. No. 2.5;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 LGDWMLNYFRLVPPGT 18
:||||:||:| : | |
Db 10 MGDWILNHFFFLLTPRT 25

Search completed: January 7, 2005, 16:19:54
Job time : 146 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2005, 15:54:26 ; Search time 21 Seconds
(without alignments)
56.844 Million cell updates/sec

Title: US-10-666-480-231
Perfect score: 104
Sequence: 1 DQLGDWMLNYFRLVPPGT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	ID
<hr/>					
1	50	48.1	557	1	US-08-309-341-2
2	50	48.1	557	1	US-08-309-341-4
3	50	48.1	557	1	US-08-608-267-2
4	50	48.1	557	1	US-08-608-267-4
5	50	48.1	557	1	US-08-608-452-2
6	50	48.1	557	1	US-08-608-452-4
7	50	48.1	557	1	US-08-608-224-2
8	50	48.1	557	1	US-08-608-224-4
9	50	48.1	557	2	US-08-967-149-2
10	50	48.1	557	2	US-08-967-149-4
11	49	47.1	344	3	US-09-298-886-11

12	49	47.1	344	4	US-09-999-672-11	Sequence 11, Appl
13	48	46.2	207	4	US-09-556-877-300	Sequence 300, App
14	48	46.2	207	4	US-09-620-412C-300	Sequence 300, App
15	48	46.2	207	4	US-09-598-419-300	Sequence 300, App
16	47	45.2	419	1	US-08-553-703A-3	Sequence 3, Appli
17	47	45.2	419	2	US-09-006-021-3	Sequence 3, Appli
18	46	44.2	417	1	US-08-553-703A-2	Sequence 2, Appli
19	46	44.2	417	2	US-09-006-021-2	Sequence 2, Appli
20	43.5	41.8	206	4	US-09-270-767-58357	Sequence 58357, A
21	43.5	41.8	367	4	US-09-270-767-43028	Sequence 43028, A
22	43	41.3	264	4	US-09-198-452A-810	Sequence 810, App
23	43	41.3	462	3	US-08-630-915A-38	Sequence 38, Appl
24	43	41.3	462	4	US-09-879-957-38	Sequence 38, Appl
25	43	41.3	520	4	US-09-538-092-1347	Sequence 1347, Ap
26	43	41.3	972	3	US-08-335-844A-23	Sequence 23, Appl
27	43	41.3	972	4	US-09-129-366-23	Sequence 23, Appl
28	42.5	40.9	481	4	US-09-489-039A-7588	Sequence 7588, Ap
29	42	40.4	904	4	US-09-543-681A-4485	Sequence 4485, Ap
30	41	39.4	324	4	US-09-248-796A-17792	Sequence 17792, A
31	41	39.4	631	4	US-09-543-681A-7023	Sequence 7023, Ap
32	41	39.4	927	4	US-09-328-352-7922	Sequence 7922, Ap
33	41	39.4	1464	3	US-09-045-360-2	Sequence 2, Appli
34	41	39.4	1464	4	US-09-713-273A-21	Sequence 21, Appl
35	41	39.4	1464	4	US-10-038-224-2	Sequence 2, Appli
36	40.5	38.9	235	4	US-09-489-039A-12012	Sequence 12012, A
37	40.5	38.9	274	4	US-09-270-767-40695	Sequence 40695, A
38	40.5	38.9	274	4	US-09-270-767-55911	Sequence 55911, A
39	40.5	38.9	677	2	US-08-522-269B-3	Sequence 3, Appli
40	40.5	38.9	677	3	US-09-294-923-3	Sequence 3, Appli
41	40	38.5	450	4	US-09-252-991A-25019	Sequence 25019, A
42	40	38.5	474	4	US-09-270-767-43583	Sequence 43583, A
43	40	38.5	551	4	US-09-248-796A-18881	Sequence 18881, A
44	40	38.5	688	4	US-09-538-092-794	Sequence 794, App
45	39.5	38.0	510	3	US-09-118-442-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-309-341-2

```
; Sequence 2, Application US/08309341
; Patent No. 5594119
; GENERAL INFORMATION:
;   APPLICANT: Yaver, Debbie Sue
;   APPLICANT: Thompson, Sheryl Ann
;   TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: No. 5594119o No. 5594119disk of No. 5594119th America, Inc.
;     STREET: 405 Lexington Avenue, Suite 6400
;     CITY: New York
;     STATE: New York
;     COUNTRY: U.S.A.
;     ZIP: 10174-6401
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/309,341
; FILING DATE: 16-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus Niger

US-08-309-341-2

Query Match 48.1%; Score 50; DB 1; Length 557;
Best Local Similarity 75.0%; Pred. No. 7.3;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GDWMLNYFRLVP 15
||||| | |||||
Db 445 GDWMKPYHRLVP 456

Search completed: January 7, 2005, 16:09:00
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2005, 15:49:26 ; Search time 154 Seconds
(without alignments)
41.929 Million cell updates/sec

Title: US-10-666-480-231
Perfect score: 104
Sequence: 1 DQLGDWMLNYFRLVPPGT 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	104	100.0	18	8 ADM17879	ADM17879 Nerve gro
2	104	100.0	20	8 ADM17869	ADM17869 Nerve gro
3	104	100.0	22	8 ADM17885	ADM17885 Nerve gro
4	104	100.0	22	8 ADM17850	ADM17850 Nerve gro
5	104	100.0	23	8 ADM17859	ADM17859 Nerve gro
6	104	100.0	23	8 ADM17920	ADM17920 Nerve gro
7	104	100.0	24	8 ADM17867	ADM17867 Nerve gro
8	99	95.2	19	8 ADM17875	ADM17875 Nerve gro
9	54	51.9	26	8 ADM17919	ADM17919 Nerve gro

10	50	48.1	26	8	ADM17874	Adm17874 Nerve gro
11	50	48.1	518	4	ABB63107	Abb63107 Drosophil
12	50	48.1	536	5	ABR38819	Abr38819 A. niger
13	50	48.1	556	2	AAR96737	Aar96737 A. niger
14	50	48.1	557	2	AAR96738	Aar96738 A. niger
15	49	47.1	344	3	AAB36106	Aab36106 Human Sec
16	49	47.1	344	6	ABG72379	Abg72379 Human Sec
17	49	47.1	344	7	ADB97786	Adb97786 Human alp
18	48	46.2	22	8	ADM17899	Adm17899 Nerve gro
19	48	46.2	164	3	AAB44991	Aab44991 Human sec
20	48	46.2	164	3	AAB44992	Aab44992 Human sec
21	48	46.2	198	2	AAY37590	Aay37590 Amino aci
22	48	46.2	207	3	AAB13696	Aab13696 Chlamydia
23	48	46.2	207	4	AAG83264	Aag83264 Protein e
24	48	46.2	207	5	ABB94235	Abb94235 Chlamydia
25	48	46.2	243	5	ABB94356	Abb94356 Chlamydia
26	48	46.2	249	5	ABB94257	Abb94257 Chlamydia
27	48	46.2	470	8	ADH22542	Adh22542 Human tra
28	48	46.2	707	4	AAM23744	Aam23744 Human EST
29	48	46.2	707	4	AAM23715	Aam23715 Human EST
30	48	46.2	896	6	ABR43913	Abr43913 Human sod
31	48	46.2	896	7	ADJ68814	Adj68814 Human hea
32	47	45.2	26	8	ADM17887	Adm17887 Nerve gro
33	47	45.2	419	2	AAR79930	Aar79930 Porcine a
34	47	45.2	654	8	ADN48015	Adn48015 Thermococ
35	47	45.2	892	6	ABM67426	Abm67426 Photorhab
36	46	44.2	291	7	ADC46699	Adc46699 Thalecre
37	46	44.2	291	8	ADO02503	Ado02503 Thalecre
38	46	44.2	417	2	AAR79929	Aar79929 Porcine a
39	45	43.3	359	5	AAM49555	Aam49555 Actinopla
40	44	42.3	21	8	ADM17858	Adm17858 Nerve gro
41	44	42.3	22	8	ADM17880	Adm17880 Nerve gro
42	44	42.3	687	4	ABB64842	Abb64842 Drosophil
43	43	41.3	26	8	ADM17861	Adm17861 Nerve gro
44	43	41.3	164	5	ABP41930	Abp41930 Human ova
45	43	41.3	246	5	ABB94321	Abb94321 Chlamydia

ALIGNMENTS

RESULT 1

ADM17879

ID ADM17879 standard; peptide; 18 AA.

XX

AC ADM17879;

XX

DT 17-JUN-2004 (first entry)

XX

DE Nerve growth factor activity modulating peptide SEQ ID NO:231.

XX

KW nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;

KW nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;

KW post-herpetic neuralgia; inflammatory pain; migraine; asthma;

KW hyperactive bladder; psoriasis; cancer; acute pain; dental pain;

KW surgical pain; pain; causalgia; demyelinating disease;

KW trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;

KW diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW chronic inflammatory condition; neuropathic pain; genitourinary; wound;
KW burn; allergic skin reaction; pruritus; vitiligo;
KW gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer.
XX
OS Synthetic.
XX
PN WO2004026329-A1.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-US029866.
XX
PR 19-SEP-2002; 2002US-0412524P.
PR 18-SEP-2003; 2003US-00666480.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boone TC, Wild KD, Sitney KC, Min H, Kimmel B;
XX
DR WPI; 2004-283150/26.
XX
PT Novel peptide capable of modulating nerve growth factor activity, useful
PT for treating disease or disorder e.g., acute pain, dental pain, cancer,
PT migraine and collagen vascular disease.
XX
PS Claim 113; SEQ ID NO 231; 267pp; English.
XX
CC The present invention describes a peptide (I) that is capable of
CC modulating nerve growth factor (NGF) activity. Also described: (1)
CC modified peptide (II) comprising (I) and a vehicle, where the modified
CC peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC (I); (3) modified peptide (III), its multimers or its salt, where the
CC peptide is capable of modulating NGF activity; (4) polynucleotide (IV)
CC encoding (I), (II) or (III); (5) expression vector (V) comprising (IV);
CC (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and
CC a vehicle, where the composition of matter is capable of modulating NGF
CC activity; and (8) pharmaceutical composition comprising (I), (II) or
CC (III) and a diluent or carrier. (I) has analgesic activity, and can be
CC used as an inhibitor of NGF. (I) is useful for treating or preventing a
CC disease or disorder associated with NGF activity by administering (I) to
CC human or animal. The disease or disorder chosen from neurologic pain,
CC painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain,
CC migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain,
CC dental pain, pain from trauma, surgical pain, pain resulting from
CC amputation or abscess, causalgia, demyelinating diseases, trigeminal
CC neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes,
CC acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy,
CC general headache, cluster headache, mixed-vascular and non-vascular
CC syndromes, tension headache, general inflammation, arthritis, rheumatic
CC diseases, lupus, osteoarthritis, inflammatory bowel disorders,
CC inflammatory eye disorders, inflammatory or unstable bladder disorders,
CC skin complaints with inflammatory components, sunburn, carditis,
CC dermatitis, myositis, neuritis, collagen vascular diseases, chronic

CC inflammatory conditions, inflammatory pain associated hyperalgesia and
CC allodynia, neuropathic pain and associated hyperalgesia and allodynia,
CC diabetic neuropathy pain, sympathetically maintained pain,
CC deafferentation syndromes, epithelial tissue damage or dysfunction,
CC herpes simplex, post-herpetic neuralgia, disturbances of visceral
CC motility at respiratory, genitourinary, gastrointestinal or vascular
CC regions, wounds, burns, allergic skin reactions, pruritus, vitiligo,
CC general gastrointestinal disorders, colitis, gastric ulceration, duodenal
CC ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is
CC also useful for modulating pain or promoting analgesia by administering
CC (I) to human or animal. (I) is also useful in the manufacture of
CC medicament for the treatment of disease or disorder. The present sequence
CC is used in the exemplification of the present invention.
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 104; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQLGDWMLNYFRLVPPGT 18
|||||||||||||||||||
Db 1 DQLGDWMLNYFRLVPPGT 18

RESULT 11

ABB63107

ID ABB63107 standard; protein; 518 AA.

XX

AC ABB63107;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 16113.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-US009231.

XX

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX

PA (PEKE) PE CORP NY.

XX

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

DR WPI; 2001-656860/75.

DR N-PSDB; ABL07210.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
XX
PS Disclosure; SEQ ID NO 16113; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 518 AA;

Query Match 48.1%; Score 50; DB 4; Length 518;
Best Local Similarity 44.4%; Pred. No. 13;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DQLGDWMLNYFRLVPPGT 18
 :|: ||| :| :: |||
Db 29 EQIERWMLEWFMVLRPGT 46

Search completed: January 7, 2005, 16:08:12
Job time : 156 secs